

**REMARKS**

Reconsideration and allowance are respectfully requested.

Claims 91-105 are now pending, with claim 91 being the sole independent claim.

Applicants have corrected the cross-reference to related applications section on page 1, lines 1-2, to correct an erroneously made priority claim and to reflect properly that the present application is a continuation of PCT/US99/06047, which claims the benefit of U.S. Provisional Application No. 60/078,948. No petition and fee is believed due, since the present application was filed prior to November 29, 2000.

A substitute Sequence Listing is filed simultaneously herewith. As explained further in the Remarks accompanying this substitute Sequence Listing, in SEQ ID NO:12, a 351 amino acid sequence (encoded by nucleotides 131-1186 of SEQ ID NO:11) replaces the originally-filed 339 amino acid sequence (encoded by nucleotides 167-1186 of SEQ ID NO:11).

A substitute Figure 2A-2B is submitted herewith. Figure 2 as originally filed contained the sequence of originally-filed SEQ ID NO:12, i.e., the 339 amino acid sequence mentioned above. The attached substitute Figure 2A-2B now contains the 351 amino acid sequence of SEQ ID NO:12 submitted in the substitute Sequence Listing filed simultaneously herewith.

A substitute Figure 3A-3B is submitted herewith. Figure 3 as originally filed erroneously contained a partial amino acid sequence of 344 residues for SEQ ID NO:18. The attached substitute Figure 3A-3B now contains, for SEQ ID NO:18, the 388 amino acid sequence of SEQ ID NO:18 as originally filed. Further basis for this amendment is found in the specification at page 3, lines 21-22, which describes Figure 3 as containing SEQ ID NO:18.

A currently amended Table 5, of Example 4, is submitted to correct the following errors in the original Table 5: 1) the original percent identities were erroneously based on a comparison to the Arabidopsis delta-1 cyclin of GI No. 1076311, instead of to the highly similar Arabidopsis delta-1 cyclin of GI No. 3915635 (SEQ ID NO:30) as stated at page 20, lines 8-13 of the specification; 2) the amino acid sequence of the currently amended SEQ ID NO:12 is used; and 3) for some sequences of the original Table 5, a "period" was used in the amino acid sequence to correspond to the stop codon; in the currently amended Table 5, all amino acid sequences used are as presented in the currently amended Sequence Listing, i.e., no periods are used to indicate the end of the protein.

A currently amended Table 7, of Example 5, is submitted to properly list the percent identity of the amino acid sequence of SEQ ID NO:18 when compared to the Nicotiana tabacum cyclin delta-2 protein (SEQ ID NO:31). The basis for this

correction is page 22, lines 5-8 and lines 27-30 of the specification. In Table 7 as originally filed, the percent identities were erroneously calculated using a partial amino acid sequence of 344 residues for SEQ ID NO:18. A spelling error in the title of Table 7 is also corrected.

No new matter is believed to have been added.

Turning now to the Office Action mailed January 2, 2003:

Regarding the combined Section 101 (utility) and Section 112, 1<sup>st</sup> paragraph (how to use) rejections, Applicants submit the following as rebuttal arguments:

First, reference is made to Appendix A, attached hereto. Appendix A contains a BLASTX analysis indicating the result shown in Table 4 of the instant specification, namely, an E-115 probability of the sequence similarity between the polypeptide encoded by SEQ ID NO:11 and the *Arabidopsis cyclin delta-1* having occurred by chance, as well as the top ten BLASTX hits, with probabilities ranging from E-115 to 8E-44, are to delta cyclins from *Arabidopsis*, *Nicotiana tabacum*, and *Chenopodium rubrum*.

Second, Clustal comparison of SEQ ID NO:12 to the *Arabidopsis cyclin delta-1* (SEQ ID NO:30) is 57% as now reflected in amended Table 5. Additionally, a pairwise Clustal alignment of the amended SEQ ID NO:12 and SEQ ID NO:30 (*Arabidopsis cyclin delta-1*) is given in Appendix B.<sup>1</sup> The pairwise alignment shows three regions of sequence identity: 1) Region A, containing amino acids 1-60 of SEQ ID NO:12, has 32% sequence identity to SEQ ID NO:30; 2) Region B, containing amino acids 61-248, has 77% sequence identity to SEQ ID NO:30; and 3) Region C, containing amino acids 249-351, has 32% sequence identity to SEQ ID NO:30. Consequently, the sequence comparison of SEQ ID NO:12 to SEQ ID NO:30 indicates a large central region of high sequence identity (77%), between smaller amino and carboxyl-terminal regions of lower sequence identity (32% each).

Third, in the amino-terminal Region A, there is the presence of an Rb-binding domain, L-X-C-X-E, that is conserved among delta cyclins. See Soni, B. et al. (1995) Plant Cell 7(1):85-103, cited in the previously submitted IDS).

In view of the foregoing, Applicants submit that one of skill in the art would expect SEQ ID NO:12 to represent a functional cyclin delta-1 protein, and therefore,

---

<sup>1</sup> In Appendix B the numbering of the consensus sequence is given below the sequence alignment. The numbering of each sequence is given to the left of each row, and to the right of the last row. Positions that contain identical amino acids in each sequence are indicated with an asterisk. Amino-terminal sequence from a related clone, scr1c.pk003.j21, is given below the sequence alignment.

respectfully request withdrawal of the combined Section 101 and Section 112, 1<sup>st</sup> paragraph rejection.

Applicants further wish to note the following. The contig of SEQ ID NO:11 encodes a protein of 351 amino acids. Amino acids 11-351 (97% of the protein) are from the cDNA insert in clone sr1.pk0001.g5, and amino acids 1-10 are from the EST sequence of clone sah1c.pk003.i7. After the filing date of the instant application, Applicants sequenced the entire cDNA insert of sah1c.pk003.i7 and determined that this clone represented a different, but highly homologous, sequence to that of sr1.pk0001.g5. Consequently, the joining of sequences from clones sr1.pk0001.g5 and sah1c.pk003.i7 created an artificial contig sequence. A different clone, scr1c.pk003.j21, from the proprietary database was found to represent the authentic 5' end of the gene represented by clone sr1.pk0001.g5. Consequently, the authentic amino-terminus for the protein 97% encoded by sr1.pk0001.g5 can be obtained from clone scr1c.pk003.j21. The authentic amino-terminus is shown in Appendix B, below the sequence alignment. Instead of the 10 amino acids, MNAEPPPLPPA, from the contig in SEQ ID NO:11, the authentic protein should have the following eight amino acids, MNAESPPG, at the amino-terminus. Because these two short sequences are very similar (six amino acids are identical), and because, in general, alterations of the N-terminal and C-terminal portions of a protein molecule would also not be expected to alter the activity of the protein (see the specification, page 6, lines 21-23), Applicants contend that one of skill in the art would expect the artificial sequence of SEQ ID NO:12 to represent a functional cyclin delta-1 protein.

Regarding the Section 112, 1<sup>st</sup> paragraph written description rejection, Applicants respectfully traverse.

Applicants submit that the specification discloses to one of ordinary skill in the art a representative number of polynucleotides encoding a polypeptide having cyclin delta activity, wherein the amino acid sequence of the polypeptide and the amino acid sequence of SEQ ID NO:12 have at least 80% sequence identity based on the Clustal alignment method.

The specification at page 6, lines 13-25, discloses alterations in nucleotide sequence that are not expected to alter functionality, such as alterations that produce a chemically equivalent amino acid at a given site or alterations in the N- or C-terminal portions. Also in the specification, at page 4, Table 4, the result (pLog = 115) of a BLASTX analysis is given for comparison of the protein encoded by SEQ ID NO:11 and the *Arabidopsis* cyclin delta-1 (SEQ ID NO:30). The sequence alignment from that BLASTX analysis is presented as Appendix C. In the alignment of Appendix C, the position of forty conservative amino acid changes are noted with "plus" signs. Thus, from the foregoing, the skilled artisan would immediately

understand the specification to disclose a representative number of polynucleotide sequences, having different nucleotide substitutions, that encode polypeptides having cyclin delta-1 enzyme activity but that vary from the 351 amino acids encoded by SEQ ID NO:11.

Withdrawal of the Section 112, 1<sup>st</sup> paragraph written description rejection is therefore respectfully requested.

Applicants believe the foregoing to be responsive to each point raised in the Office Action. A Notice of Allowance is respectfully requested.

Please charge any fees or credit any overpayment of fees which are required in connection herewith to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

Applicants' undersigned may be reached at the below-listed numbers.

Respectfully submitted,



J. KENNETH JOUNG  
Attorney For Applicants  
Registration No. 41,881  
Telephone: 302-992-4929  
Facsimile: 302-892-1026

Dated: 2 July 2003

Enclosures: Appendices A, B & C  
Substitute Figures 2A-2B and 3A-3B

## APPENDIX A

BLASTX 2.0.6 [Sept-16-1998]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= sahlc.pk003.i7 (2259 letters)	2/16/99 no filter, Becky
---	--------------------------

Database: /blast/data/2.0/2/nr  
356,412 sequences; 108,900,843 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value	N	plog
gi 3915635 sp P42751 CGD1_ARATH CYCLIN DELTA-1 >gi 2995130 g...	357	e-115	4	115.00
gi 2194121 (AC002062) Strong similarity to Arabidopsis cycli...	357	e-113	3	113.00
gi 1076311 pir  SS1650 cyclin delta-1 - Arabidopsis thaliana	277	1e-91	4	
gi 4160300 gnl PID e1370827 (AJ011893) cyclin D3.1 protein [...	197	4e-49	1	
gi 4160298 gnl PID e1370825 (AJ011892) cyclin D2.1 protein [...	193	7e-48	1	
gi 3915637 sp P42753 CGD3_ARATH CYCLIN DELTA-3 >gi 2995134 g...	186	6e-46	2	
gi 1076313 pir  SS1652 cyclin delta-3 - Arabidopsis thaliana	186	6e-46	2	
gi 2911046 gnl PID e1253334 (AL021961) cyclin delta-3 [Arabi...	186	8e-46	2	
gi 1770190 gnl PID e290219 (Y10162) cyclin-D like protein [C...	123	1e-45	3	
gi 1076312 pir  SS1651 cyclin delta-2 - Arabidopsis thaliana	169	8e-44	3	
>gi 3915635 sp P42751 CGD1_ARATH CYCLIN DELTA-1 >gi 2995130 gnl PID e1284155 (X83369) cyclin delta-1 [Arabidopsis thaliana] Length = 335				
Score = 38.2 bits (77), Expect(4) = e-115 Identities = 199/307 (64%), Positives = 239/307 (77%)				
Query: 161 LLMSVSCLSDYDLGEDSSGILSGESPECFSIDSSP 277 L MSVS +D DL CGEDS + + S S++DS P Sbjct: 10 LHMSVFSNDMDLFCGEDSGVFSGESTVDFSSSEVDSWP 48				
Score = 357 bits (774), Expect(4) = e-115 Identities = 181/268 (67%), Positives = 216/268 (80%)				
Query: 311 SIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYM 490 SIA FIE ER+FVPG +YLSRFQ+RSLDA+ARE+SV WILKV AYY FQPLTAYLAVNYM Sbjct: 51 SIACFIEDERHFVPGHDYLSRFQTRSLDASAREDSVAWILKVQAYYNFQPLTAYLAVNYM 110				
Query: 491 DRFLDSRRLPETNGWPLQLVSVACLSLAALKMEEPLVPSLLDQIEGAKYIFEPRTIRRME 670 DRFL +RRLPET+GWP+QL++VACLSLAALKMEE LVPSL D Q+ G KY+FE +TI+RME Sbjct: 111 DRFLYARRLPETSGWPMQLLAVACLSLAALKMEEILVPSLFDFQAGVKYLFEAKTIKRME 170				
Query: 671 LLVLGVLDWRRLRSVTPLCFLAFFACKVDSTGTFLISRATEIIIVSNIQEASFLAYWPS 850 LLVL VLDWRRLRSVTP F++FFA K+D +GTF+ F IS ATEII+SNI+EASFL YWPS Sbjct: 171 LLVLGVLDWRRLRSVTPLFISFFAYKIDPSGTFLGFFISHATEIILSNIKEASFLAYWPS 230				
Query: 851 CIAAAAILTAANEIPNWSVV 910 IAAAAIL ANE+P+ S V Sbjct: 231 SIAAAAILCVANELPSLSSV 250				

## APPENDIX A (continued)

Score = 53.3 bits (110), Expect(4) = e-115  
Identities = 31/68 (45%), Positives = 43/68 (62%)

Query: 917 ENAESWCEGLRKEKVIGCYQLMQUELVINNNQRKLP 1021  
E+ E+WC+GL KEK++ CY+LM+ + I NN+ P  
Sbjct: 255 ESPETWCDGLSKEKIVRCYRLMKAMAIENNRLNTP 289

Score = 29.0 bits (57), Expect(4) = e-115  
Identities = 14/33 (42%), Positives = 17/33 (51%)

Query: 1073 SSTVSSFSSSSSTSFSLSCKRRKLNNRLWVDDK 1171  
S SS + S S CKRRKL+ WV D+  
Sbjct: 298 SVRASSTLTRPSDESSSPCKRRKLSGYSWVGDE 330

>gi|2194121 (AC002062) Strong similarity to Arabidopsis cyclin delta-1  
(gb|ATCD1). EST gb|ATTS4338 comes from this gene.  
[Arabidopsis thaliana]  
Length = 339

Score = 38.2 bits (77), Expect(3) = e-113  
Identities = 208/336 (61%), Positives = 255/336 (74%)

Query: 161 LLMSVSCLSDYDLCGEDSSGILSGESPECFSIDSSP 277  
L MSVS +D DL CGEDS + + S S++DS P  
Sbjct: 10 LHMSVFSNDMDLFCGEDSGVFSGESTVDFSSEVDSWP 48

Score = 357 bits (774), Expect(3) = e-113  
Identities = 190/297 (63%), Positives = 232/297 (77%)

Query: 311 SIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYM 490  
SIA FIE ER+FVPG +YLSRFQ+RSLDA+ARE+SV WILKV AYY FQPLTAYLAVNYM  
Sbjct: 51 SIACFIEDERHFVPGHDYLSRFQTRSLDASAREDVAWILKVQAYYNFQPLTAYLAVNYM 110

Query: 491 DRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLLQIEGAKYIFEPRPTIRRME 670  
DRFL +RRLPET+GWP+QL++VACLSLAAKMEE LVPSL D Q+ G KY+FE +TI+RME  
Sbjct: 111 DRFLYARRLPETSGWPMQLLAVACLSLAAKMEEILVPSLFDFQVAGVKYLFEAKTIKRME 170

Query: 671 LLVLGVLDWRRLRSVTPLCFLAFFACKVDSTGT FIRFLISR RATEII VSNI QEASFLAYWPS 850  
LLVL VLDWRRLRSVTP F++FFA K+D +GTF+ F IS ATEII+SNI+EASFL YWPS  
Sbjct: 171 LLVLSVLDWRRLRSVTPLFDISFFAYKIDPSGTFLGFFISHATEIILSNIKEASFLEYWPS 230

Query: 851 CAAAAAILTAANEIPNWSVV 910  
IAAAAIL ANE+P+ S V  
Sbjct: 231 SIAAAAILCVANELPSLSSV 250

Score = 56.5 bits (117), Expect(3) = e-113  
Identities = 40/97 (41%), Positives = 59/97 (60%)

Query: 917 ENAESWCEGLRKEKVIGCYQLMQUELVINNNQRKLP 1096  
E+ E+WC+GL KEK++ CY+LM+ + I NN+ P + ++ V + + + S  
Sbjct: 255 ESPETWCDGLSKEKIVRCYRLMKAMAIENNRLNTPKVIAKLRSVRASSTLTRPSDESSF 314

Query: 1097 SSSS 1108  
SSSS  
Sbjct: 315 SSSS 318

Score = 36.8 bits (74), Expect = 1.0  
Identities = 17/33 (51%), Positives = 21/33 (63%)

Query: 1073 SSTVSSFSSSSSTSFSLSCKRRKLNNRLWVDDK 1171  
SST++ S SS S S CKRRKL+ WV D+  
Sbjct: 302 SSTLTRPSDESSPSSSPCKRRKLSGYSWVGDE 334

## APPENDIX A (continued)

```
>gi|1076311|pir||S51650 cyclin delta-1 - Arabidopsis thaliana
Length = 334

Score = 38.2 bits (77), Expect(4) = 1e-91
Identities = 174/312 (55%), Positives = 215/312 (68%)

Query: 161 LLMSVSCLSDYDLCGEDSSGILSGESPECFSFSDIDSSP 277
      L MSVS +D DL CGEDS + + S S++DS P
Sbjct: 10  LHMSVFSNDMDLFCGEDSGVFSGESTVDFSSSEVDSWP 48

Score = 277 bits (599), Expect(4) = 1e-91
Identities = 156/273 (57%), Positives = 192/273 (70%)

Query: 311 SIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYM 490
      SIA FIE ER FVPG +YLSRFQ+RSLDA+ARE+SV WILKV AYY FQPL+AYLAVNYM
Sbjct: 51  SIACFIEDERTFVPGHDYLSRFQTRSLDASAREDVAWILKVQAYYNFQPLSAYLAVNYM 110

Query: 491 DRFLDSRRLPETNGWPLQLVSVACLSLAAKMEEPLVPSLDDLQIEGAKYIFEPRTIRRME 670
      DRFL +RRLPET+GWP+QL+ +VACLSLAAKMEE LVPSL D Q+ G KY+FE +TI+RME
Sbjct: 111 DRFLYARRLPETSGWPMQLLAVACLSLAAKMEEILVPSLFDFQVAGVKYLFEAKTIKRME 170

Query: 671 LLVLGVLDWRRLRSVTPLCFLAFFACKVDSTGT FIRFLISRATIEIVSNIQEASFLAYWPS 850
      LLVL VLDWRRLRSVT P F++FFA K+D F L I+ + + + + S
Sbjct: 171 LLVLSVLDWRRLRSVT PFDISFFAYKIDL RVPFSGSLSIPLQSIKESFLEYWPSS 230

Query: 851 CIAAAAILTAANEIPNWSVVKPENA 925
      AAA + A SVV P +
Sbjct: 231 IAAAAILCVANELPSLSSVVNPHEs 255

Score = 53.3 bits (110), Expect(4) = 1e-91
Identities = 31/68 (45%), Positives = 43/68 (62%)

Query: 917 ENAESWCEGLRKEKVIGCYQLMQUELVINNNQRKLP 1021
      E+ E+WC+GL KEK++ CY+LM+ + I NN+ P
Sbjct: 254 ESPETWCDGLSKEKIVRCYRLMKAMAIENNRLNTP 288

Score = 29.0 bits (57), Expect(4) = 1e-91
Identities = 14/33 (42%), Positives = 17/33 (51%)

Query: 1073 SSTVSSFSSSSSTSFSLSCKRRKLNNRNLWVDDK 1171
      S SS + S S CKRRKL+ WV D+
Sbjct: 297 SVRASSTLTRPSDESSSPCKRRKLSGYSWVGDE 329

>gi|4160300|gnl|PID|e1370827 (AJ011893) cyclin D3.1 protein [Nicotiana tabacum]
Length = 373

Score = 197 bits (425), Expect = 4e-49
Identities = 90/210 (42%), Positives = 126/210 (59%)

Query: 362 YLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPL 541
      + + FQ SL +AR +SV WILKV+ YYGF LTA LA-NY DRFL S + W +
Sbjct: 89 WFNSFQDDSLLCSARVDSVEWILKVHAYYGFQPLTSLHYQKDWPWMI 148

Query: 542 QLVSVACLSLAAKMEEPLVPSLDDLQIEGAKYIFEPRTIRRME LLVGVLDWRRLRSVTPL 721
      QL +V CLS LAAK+EE VP LLD Q+E AKY+FE +TI+RME LLV L WR+ VTPL
Sbjct: 149 QLAATVCLSLAAKVEETQVPLLLDFQVEDAKYVFEAKTIQRMELLVLSSLKWRMNPVTPL 208

Query: 722 CFLAFFACKVDSTGT FIRFLISRATIEIVSNIQEASFLAYWPS CIIAAAILTAANEIPNW 901
      FL ++ + R + + + S + + F+ Y PS +A A +L + ++
Sbjct: 209 SFLDHIIRRLGLRNNIHWEFLRCENLLSIMADCRFVRYMPSVLATAIMLHVIHQVEPC 268

Query: 902 SVVKPENAESWCEGLRKEKVIGCYQLMQUEL 991
      + V +N + KEKV C++L+ E+
Sbjct: 269 NSVDYQNQLLGVLKINKEKVNNCFELISEV 298
```

## APPENDIX A (continued)

>gi|4160298|gnl|PID|e1370825 (AJ011892) cyclin D2.1 protein [Nicotiana tabacum]  
Length = 354  
  
Score = 193 bits (416), Expect = 7e-48  
Identities = 83/193 (43%), Positives = 127/193 (65%)  
  
Query: 314 IASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMD 493  
++ ++ E F+P +Y+ R +S LD + R+E++ WILK H +YGF L+ L++NY+D  
Sbjct: 66 LSFMVQREMEFLPKDDYVERLRSRSGDLDLSVRKEALDWILKAHMHYGFGELSFCLSINYLD 125  
  
Query: 494 RFLDSRRLPETNGWPLQLVSACLSLAAKMEEPLVPSLLDLQIEGAKYIFEPRTRRMEL 673  
RFL LP + W +QL++VACLSLAAKMEE VP +DLQ+ K++FE +TI+RMEL  
Sbjct: 126 RFLSLYELPRSKTWTQVLLAVACLSLAAKMEEINVPLTVVDLQVGDPKFVFEGKTIQRMEL 185  
  
Query: 674 LVLGVLDWRRLRSVTPLCFLAFFACKVVDSTGT FIRFLISRATEIIIVSNIQEASFLAYWPSC 853  
LVL L WR+++ TP F+ +F K++ R LIS + ++I+S I+ FL + S  
Sbjct: 186 LVLSTLKWRMQAYTPYTFIDYFMRKMNGDQIPSRPLISGSMQLILSIIIRSDFLEFRSSE 245  
  
Query: 854 IAAAILTAANEI 892  
IAA+ ++ + EI  
Sbjct: 246 IAASVAMSVSGEI 258  
  
>gi|3915637|sp|P42753|CGD3\_ARATH CYCLIN DELTA-3 >gi|2995134|gnl|PID|e1284159 (X83371)  
cyclin delta-3  
[Arabidopsis thaliana]  
Length = 376  
  
Score = 186 bits (401), Expect(2) = 6e-46  
Identities = 92/235 (39%), Positives = 143/235 (60%)  
  
Query: 404 REESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSACLSLAAKM 583  
R+E+VGWIL+V+A+YGF L A LA+ Y+D+F+ S L W LQLVSACLSLAAK+  
Sbjct: 87 RKEAVGWILRVNAHYGFSTLAAVLAITYLDKFICSYSLQRDKPWMLQLVSACLSLAAKV 146  
  
Query: 584 EEPPLVPSLLDLQIEGAKYIFEPRTRRMELLVLGVLDWRRLRSVTPLCFLAFFACKVVDSTG 763  
EE VP LLD Q+E KY+FE +TI+RMELL+I L+W++ +TP+ F+ ++  
Sbjct: 147 EETQVPLLLDFQVEETKYVPEAKTIQRMELLILSTLEWKMHЛИTPISFVDHIIRRLGLKN 206  
  
Query: 764 TFIRFLISRATEIIIVSNIQEASFLAYWPSCIAAAAILTAANEI PNWSVVKPENAESWCEG 943  
+++ +++S I ++ F+ Y PS +AAA ++ ++ + + +  
Sbjct: 207 NAHDWFLNKCHRLLLSSVSDSRFVGYLPSVVAATMMRIIEQVDPFDPLSYQTNLLGVLN 266  
  
Query: 944 LRKEKVIGCYQLMQELVIN 1000  
L KEKV CY L+ +L ++  
Sbjct: 267 LTKEKVVKTCYDLILQLPVD 285  
  
Score = 20.8 bits (39), Expect(2) = 6e-46  
Identities = 12/36 (33%), Positives = 19/36 (52%)  
  
Query: 1022 LLKVLQPQLRVTTTRTRMRSSSTVSSFSSSSTSFSLSC 1129  
L+ LP R+ + +++SS SSS+ S SC  
Sbjct: 278 LILQLPVDRICLQIQSSKKRKSHDSSSSLNSPSC 313  
  
>gi|1076313|pir||S51652 cyclin delta-3 - Arabidopsis thaliana  
Length = 376  
  
Score = 186 bits (401), Expect(2) = 6e-46  
Identities = 92/235 (39%), Positives = 143/235 (60%)  
  
Query: 404 REESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSACLSLAAKM 583  
R+E+VGWIL+V+A+YGF L A LA+ Y+D+F+ S L W LQLVSACLSLAAK+  
Sbjct: 87 RKEAVGWILRVNAHYGFSTLAAVLAITYLDKFICSYSLQRDKPWMLQLVSACLSLAAKV 146

## APPENDIX A (continued)

Query: 584 EEPPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTG 763  
EE VP LLD Q+E KY+FE +TI+RMELL+L L+W++ +TP+ F+ ++  
Sbjct: 147 EETQVPLLLDFQVEETKYVFEAKTIQRMELLILSTLEWKMHЛИTPIFVDHIIIRRLGLKN 206

Query: 764 TFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIPNWSVVKPENAESWCEG 943  
+++ +++S I ++ F+ Y PS +AAA ++ ++ + + +  
Sbjct: 207 NAHWDFLNKCHRLLLSVISDSRFVGYLPSVAAATMMRIIEQVDPFDPLSYQTNLLGVLN 266

Query: 944 LRKEKVIGCYQLMQELVIN 1000  
L KEKV CY L+ +L ++  
Sbjct: 267 LTKEKVKTCTYDILQLPVD 285

Score = 20.8 bits (39), Expect(2) = 6e-46  
Identities = 12/36 (33%), Positives = 19/36 (52%)

Query: 1022 LLKVLQPQLRVTTTRMRSSSTVSSFSSSSTSFSLSC 1129  
L+ LP R+ + +++SS SSS+ S SC  
Sbjct: 278 LILQLPVDRICLQIQIQQSSKKRKSHDSSSSLNSPSC 313

>gi|2911046|gnl|PID|e1253334 (AL021961) cyclin delta-3 [Arabidopsis thaliana]  
Length = 376

Score = 186 bits (401), Expect(2) = 8e-46  
Identities = 92/235 (39%), Positives = 143/235 (60%)

Query: 404 REESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPLQLVSVACLSLAAKM 583  
R+E+VGWIL+V+A+YGF L A LA+ Y+D+F+ S L W LQLVSVACLSLAAK+  
Sbjct: 87 RKEAVGWILRVNAHYGFSTLAAVLAITYLDKFICSYSLQRDKPWMLQLVSVACLSLAAKV 146

Query: 584 EEPPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSVTPLCFLAFFACKVDSTG 763  
EE VP LLD Q+E KY+FE +TI+RMELL+L L+W++ +TP+ F+ ++  
Sbjct: 147 EETQVPLLLDFQVEETKYVFEAKTIQRMELLILSTLEWKMHЛИTPIFVDHIIIRRLGLKN 206

Query: 764 TFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAANEIPNWSVVKPENAESWCEG 943  
+++ +++S I ++ F+ Y PS +AAA ++ ++ + + +  
Sbjct: 207 NAHWDFLNKCHRLLLSVISDSRFVGYLPSVAAATMMRIIEQVDPFDPLSYQTNLLGVLN 266

Query: 944 LRKEKVIGCYQLMQELVIN 1000  
L KEKV CY L+ +L ++  
Sbjct: 267 LTKEKVKTCTYDILQLPVD 285

Score = 20.3 bits (38), Expect(2) = 8e-46  
Identities = 12/36 (33%), Positives = 19/36 (52%)

Query: 1022 LLKVLQPQLRVTTTRMRSSSTVSSFSSSSTSFSLSC 1129  
L+ LP R+ + +++SS SSS+ S SC  
Sbjct: 278 LILQLPVDRIGLQIQIQQSSKKRKSHDSSSSLNSPSC 313

>gi|1770190|gnl|PID|e290219 (Y10162) cyclin-D like protein [Chenopodium rubrum]  
Length = 372

Score = 80.8 bits (170), Expect(3) = 1e-45  
Identities = 92/221 (41%), Positives = 142/221 (63%)

Query: 314 IASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMD 493  
+AS ++ER G +YL RF++ LD AR + WI KV ++Y F PL YL+VNY+D  
Sbjct: 79 LASLFDRNERQHFLGLDYLKFRNGDLDLGARNLVIDWIHKVQSHYNFGPLCVYLSVNYLD 138

Query: 494 RFLDSRRLP 520  
RFL + LP  
Sbjct: 139 RFLSAYELP 147

## APPENDIX A (continued)

Score = 123 bits (264), Expect(3) = 1e-45  
Identities = 60/152 (39%), Positives = 98/152 (64%)

Query: 533 WPLQLVSVACLSLAALKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMELLVLGVLDWRRLRSV 712  
W +QL+ VACLSLAAK+E VP +LDLQ+ +K++FE +TI+RMELLVI L WR++SV  
Sbjct: 151 WMMQILLGVALCLSLAAKVDETDPVPLILDLQVSESKFVFEAKTIQRMELLVLSTLKWRMQSV 210

Query: 713 TPLCFLAFFACKV DSTGT FIRFLIS RATEII VSNI QEA SFLAY WPSCIAAAA ILTAANE 889  
TP F+ +F K+ + LI +A ++I+S I+ + + PS IAAA ++ +  
Sbjct: 211 TPFSFIDYFLYKLGSQDKMP SKSLIFQAIQLILSTIKGIDLMFRPSEIAAV AISVTQQ 269

Score = 19.8 bits (37), Expect(3) = 1e-45  
Identities = 7/33 (21%), Positives = 18/33 (54%)

Query: 944 LRKEK VIGCYQLM QELV INNNQRK LPLLKVLPQ 1042  
+ KE+++ C ++M +L +++ +PQ  
Sbjct: 287 VEKERLMKCVEIMHDLR MSSRSNGALASTSVPQ 319

>gi|1076312|pir||S51651 cyclin delta-2 - *Arabidopsis thaliana*  
Length = 383

Score = 169 bits (364), Expect(3) = 8e-44  
Identities = 96/232 (41%), Positives = 144/232 (61%)

Query: 314 IASFIEHERNFVPGFEYLSRFQSRSL DANAREESVGWILKVHAYGFQPLTAYLAVNYMD 493  
I + E F PG +Y+ R S LD + R +++ WILKV A+Y F L L++NY+D  
Sbjct: 67 IKEMLVREIEFCPGTDYVKRLLSGDLDLSVRNQALDWILKVCAHYHFGHLCICLSMNYLD 126

Query: 494 RFLDSRRLPETNGWPLQLVSVACLSLAALKMEEPLVPSLLDLQIEGAKYIFEPRTIRRMEL 673  
RFL S LP+ W QL++V+CLS LA+KME VP ++DLQ+E K++FE +TI+RMEL  
Sbjct: 127 RFLTSYELPKDKDWAQLLAVSCLSLASKMEETDVPHIVDLQVEDPKFVFEAKTIKRMEL 186

Query: 674 LVLGVL DWRLRSV TPLCFLAFFACKV 751  
LV+ L+WRL+++TP F+ +F K+  
Sbjct: 187 LVVTTLNWRLQALTPFSFIDYFVDKI 212

Score = 27.6 bits (54), Expect(3) = 8e-44  
Identities = 27/86 (31%), Positives = 44/86 (50%)

Query: 779 LISRATEII VSNI QEA SFLAY WPSCIAAAA ILTAA 883  
LI R++ I++ + FL + PS IAAA ++ +  
Sbjct: 220 LIYRSSR FILNTTKAIEFLDFRPSEIAAA AVS VS 254

Score = 21.2 bits (40), Expect(3) = 8e-44  
Identities = 14/51 (27%), Positives = 22/51 (42%)

Query: 860 AAA ILTAANEIPNWSVVKPENAESWC EGLRKEK VIGCYQLM QELV INNNQR 1012  
AAA + + + E A S +++B+V C LM+ L N R  
Sbjct: 246 AAAA AVS VS IS GETECIDEEKALSS LIYVKQERVKRCNL NMRSLTGEENVR 296

APPENDIX B

## APPENDIX C

```
>gi|3915635|sp|P42751|CGD1_ARATH CYCLIN DELTA-1 >gi|2995130|gnl|PID|e1284155 (X83369) cyclin delta-1  
[Arabidopsis thaliana]  
Length = 335  
  
Score = 38.2 bits (77), Expect (4) = e-115  
Identities = 199/307 (64%), Positives = 239/307 (77%)  
  
Query: 161 LIMSVSCLSDYDLICGEDSSGILSGESPECFSFDIDSSP 277  
          L MSVS +D DL CGEDS + + S S+DS P  
Sbjct: 10 LHMSVFSNSNDMLFCGEDSGVFSGESTVDFSSSEVDSWP 48  
  
Score = 357 bits (774), Expect (4) = e-115  
Identities = 181/268 (67%), Positives = 216/268 (80%)  
  
Query: 311 SIASFLEHERNFVPGFEYLRSRQFQSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYM 490  
          SIA FILE ER+FVFG +YLSRFQ+RSLDA+ARE+SV WILKV AYY FQPLTAYLAVNYM  
Sbjct: 51 SIACFIEDERHFVPGHDYLSRFQTRSLSLDASAREDSVAWILKVQAYYNFQPLTAYLAVNYM 110  
  
Query: 491 DRFLDSRRLPETNGWPLQLVSVAACLSAAKMEEPLVPSLDDLQIEGAKYIIFEPRTRRME 670  
          DRFL +RRLPET+GWP+QL++VACLSAAKME LVPSL D Q+ G KY+FE +TI+RME  
Sbjct: 111 DRFLYARRLPETSGWPMQLLAVACLSAAKMEEILVPSLFDQVAGVKYLFEAKTIKRME 170  
  
Query: 671 LLVLGVILDWRRLRSVTPLCFLAFACKVDSTGT FIRFLISRATEILIVSNIQEASFLAYWPS 850  
          LLVL VLDWRRLRSVT P F++FFA K+D + GTF+ F IS ATEII+SNI+EASFV YWPS  
Sbjct: 171 LLVLGVILDWRRLRSVT PFDISFFAYKIDPSGTFLGFFFI SHATEIILSNIKEASFLLEYWPS 230  
  
Query: 851 CTTAAAILTAANEIPNWSVV 910  
          TAAAIL ANE+P+ S V  
Sbjct: 231 STAAAILCYANEIPSLSSV 250
```

## APPENDIX C (continued)

Score = 53.3 bits (110), Expect(4) = e-115  
Identities = 31/68 (45%), Positives = 43/68 (62%)

Query: 917 ENAESWCEGLRKEKIVIGCYQLMQELVINNNQRKLP 1021  
E+ E+WC+GL KEK++ CY+LM+ + I NN+ P  
Sbjct: 255 ESPETWCDGSLSKERKIVRCYRLMKAMAIEENNRLNTP 289

Score = 29.0 bits (57), Expect(4) = e-115  
Identities = 14/33 (42%), Positives = 17/33 (51%)

Query: 1073 SSTVSSFSSSSSTSFSLSCKRKLNRLWDDK 1171  
S SS + S S CKRKL+ WV D+  
Sbjct: 298 SVRASSTLTRPSDESSSPCKRKLSGYSWVGDE 330